

SEQUENCE LISTING

<110> Hellerqvist, Carl
Fu, Changlin

<120> GBS Toxin Receptor

<130> CARB-008/01US

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<150> 60-693,843

<151> 1998-07-22

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<170> PatentIn Ver. 2.0

<210> 1

<211> 2602

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58)..(1542)

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Met Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser
1 5 10 15

acg gac cgc acg cct ctt cta ccg ggc gcc cca cgg gcc gaa gcc gct 153
Thr Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala
20 25 30

cca gtg tgc tgc tct gct cgt tac aac tta gca att ttg gcc ttt ttt 201
Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe
35 40 45

ggc ttc ttc att gtg tat gca tta cgt gtg aat ctg agt gtt gcg tta 249
Gly Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu
50 55 60

gtg gat atg gta gat tca aat aca act tta gaa gat aat aga act tcc 297

Val	Asp	Met	Val	Asp	Ser	Asn	Thr	Thr	Leu	Glu	Asp	Asn	Arg	Thr	Ser	
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aag gcg tgt cca gag cat tct gct ccc ata aaa gtt cat cat aat caa															345	
Lys Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln																
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Thr Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu																
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gg tcc ttt ttt tat ggc tac atc atc aca cag att cct gga gga tat															441	
Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr																
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gtt gcc agc aaa ata ggg ggg aaa atg ctg cta gga ttt ggg atc ctt															489	
Val Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu																
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ggc act gct gtc ctc acc ctg ttc act ccc att gct gca gat tta gga															537	
Gly Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly																
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gtt gga cca ctc att gta ctc aga gca cta gaa gga cta gga gag ggt															585	
Val Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly																
			165												175	
gtt aca ttt cca gcc atg cat gcc atg tgg tct tct tgg gct ccc cct															633	
Val Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro																
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ctt gaa aga agc aaa ctt ctt agc att tcg tat gca gga gca cag ctt															681	
Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu																
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ggg aca gta att tct ctt cct tct gga ata att tgc tac tat atg															729	
Gly Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met																
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aat tgg act tat gtc ttc tac ttt ttt ggt act att gga ata ttt tgg															777	
Asn Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp																
			225												240	
ttt ctt ttg tgg atc tgg tta gtt agt gac aca cca aaa cac aag															825	
Phe Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys																
			245												255	
aga att tcc cat tat gaa aag gaa tac att ctt tca tca tta aga aat															873	

Arg Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn				
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cag ctt tct tca cag aag tca gtg ccg tgg gta ccc att tta aaa tcc				921
Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser				
275	280	285		
ctg cca ctt tgg gct atc gta gtt gca cac ttt tct tac aac tgg act				969
Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr				
290	295	300		
ttt tat act tta ttg aca tta ttg cct act tat atg aag gag atc cta				1017
Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu				
305	310	315	320	
agg ttc aat gtt caa gag aat ggg ttt tta tct tca ttg cct tat tta				1065
Arg Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu				
325	330	335		
ggc tct tgg tta tgt atg atc ctg tct ggt caa gct gct gac aat tta				1113
Gly Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu				
340	345	350		
agg gca aaa tgg aat ttt tca act tta tgt gtt cgc aga att ttt agc				1161
Arg Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser				
355	360	365		
ctt ata gga atg att gga cct gca gta ttc ctg gta gct gct ggc ttc				1209
Leu Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe				
370	375	380		
att ggc tgt gat tat tct ttg gcc gtt gct ttc cta act ata tca aca				1257
Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr				
385	390	395	400	
aca ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat				1305
Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp				
405	410	415		
att gct cct tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt				1353
Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe				
420	425	430		
gcc act att cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc				1401
Ala Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr				
435	440	445		
cct gat aac act gtt gga gaa tgg caa acc gtg ttc tat att gct gct				1449

Pro Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala
450 455 460

gct att aat gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt 1497
Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly
465 470 475 480

gaa gta caa aac tgg gct ctc aat gat cac cat gga cac aga cac 1542
Glu Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His
485 490 495

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<211> 495

<212> PRT

<213> Homo sapiens

<400> 2

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Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe
35 40 45

Gly Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu
50 55 60

Val Asp Met Val Asp Ser Asn Thr Thr Leu Glu Asp Asn Arg Thr Ser
65 70 75 80

Lys Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln
85 90 95

Thr Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu
100 105 110

Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr
115 120 125

Val Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu
130 135 140

Gly Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly
145 150 155 160

Val Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly
165 170 175

Val Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro
180 185 190

Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu
195 200 205

Gly Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met
210 215 220

Asn Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp
225 230 235 240

Phe Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys
245 250 255

Arg Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn
260 265 270

Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser
275 280 285

Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr
290 295 300

Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu
305 310 315 320

Arg Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu
325 330 335

Gly Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu
340 345 350

Arg Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser
355 360 365

Leu Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe
370 375 380

Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr
385 390 395 400

Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp
405 410 415

Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe
420 425 430

Ala Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr
435 440 445

Pro Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala
450 455 460

Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly
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485 490 495

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<213> Ovis sp.

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<222> (84)..(1568)

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Met Lys Ser Pro Val Ser Asp Leu Ala Pro
1 5 10

agc gac ggc gag gag ggc tcg gac cgc aca ccg ctc ctg cag cgc gcc 161
Ser Asp Gly Glu Gly Ser Asp Arg Thr Pro Leu Leu Gln Arg Ala
15 20 25

ccg cgg gcg gaa ccc gct cca gta tgc tgc tct gct cgt tac aac cta 209
Pro Arg Ala Glu Pro Ala Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu
30 35 40

gca ttt ttg tcc ttt ttt ggt ttc ttc gtt ctc tat tca tta cgg gtg 257
Ala Phe Leu Ser Phe Phe Gly Phe Phe Val Leu Tyr Ser Leu Arg Val
45 50 55

aat ctg agc gtt gca cta gtg gac atg gtg gat tca aac aca act gcc 305
Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn Thr Thr Ala
60 65 70

aaa gat aat aga acg tcc tac gag tgt gca gag cat tct gct ccc ata 353
Lys Asp Asn Arg Thr Ser Tyr Glu Cys Ala Glu His Ser Ala Pro Ile
75 80 85 90

aaa gtt ctt cac aac caa acg ggt aaa aag tac cgg tgg gat gca gaa 401
Lys Val Leu His Asn Gln Thr Gly Lys Lys Tyr Arg Trp Asp Ala Glu
95 100 105

act caa gga tgg att ctc gga tct ttt ttc tat ggc tac atc atc aca 449
Thr Gln Gly Trp Ile Leu Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr
110 115 120

caa att cct gga gga tat gtt gcc agc aga agt ggg ggg aag ctg ttg			497
Gln Ile Pro Gly Gly Tyr Val Ala Ser Arg Ser Gly Gly Lys Leu Leu			
125	130	135	
ctc gga ttc ggg atc ttt gct aca gct atc ttc acc ctg ttc act ccc			545
Leu Gly Phe Gly Ile Phe Ala Thr Ala Ile Phe Thr Leu Phe Thr Pro			
140	145	150	
ctc gct gca gat ttc gga gtc gga gcc ctt gtt gca ctc agg gca cta			593
Leu Ala Ala Asp Phe Gly Val Gly Ala Leu Val Ala Leu Arg Ala Leu			
155	160	165	170
gaa ggg cta gga gag ggt gtc aca tat cca gcc atg cat gcc atg tgg			641
Glu Gly Leu Gly Glu Gly Val Thr Tyr Pro Ala Met His Ala Met Trp			
175	180	185	
tct tca tgg gct ccc cct ctt gaa aga agc aag ctt ctg agt att tca			689
Ser Ser Trp Ala Pro Pro Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser			
190	195	200	
tat gca gga gca caa ctt ggg aca gta gtt tct ctt cct ctt tct gga			737
Tyr Ala Gly Ala Gln Leu Gly Thr Val Val Ser Leu Pro Leu Ser Gly			
205	210	215	
gta att tgc tac tat atg aat tgg act tat gtc ttc tat ttc ttt ggc			785
Val Ile Cys Tyr Tyr Met Asn Trp Thr Tyr Val Phe Tyr Phe Gly			
220	225	230	
att gtt gga atc atc tgg ttt att tta tgg atc tgc tta gtt agt gat			833
Ile Val Gly Ile Ile Trp Phe Ile Leu Trp Ile Cys Leu Val Ser Asp			
235	240	245	250
aca cca gaa act cac aag aca atc act ccc tat gaa aag gag tat att			881
Thr Pro Glu Thr His Lys Thr Ile Thr Pro Tyr Glu Lys Glu Tyr Ile			
255	260	265	
ctt tca tca tta aaa aat cag ctc tct tca cag aag tca gtg ccg tgg			929
Leu Ser Ser Leu Lys Asn Gln Leu Ser Ser Gln Lys Ser Val Pro Trp			
270	275	280	
ata cct atg ctg aaa tca ctg cca ctt tgg gct att gtc gtt gca cat			977
Ile Pro Met Leu Lys Ser Leu Pro Leu Trp Ala Ile Val Val Ala His			
285	290	295	
ttt tct tac aac tgg act ttt tat act ttg ttg acc tta ttg cct act			1025
Phe Ser Tyr Asn Trp Thr Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr			
300	305	310	

tac atg aag gaa gtc cta agg ttc aat att caa gag aat ggg ttt tta			1073
Tyr Met Lys Glu Val Leu Arg Phe Asn Ile Gln Glu Asn Gly Phe Leu			
315	320	325	330
tct gca gtc cct tat tta ggt tgt tgg tta tgt atg atc ctg tcg ggt			1121
Ser Ala Val Pro Tyr Leu Gly Cys Trp Leu Cys Met Ile Leu Ser Gly			
335	340	345	
caa gct gct gac aat tta agg gca aga tgg aat ttt tca act ctg tgg			1169
Gln Ala Ala Asp Asn Leu Arg Ala Arg Trp Asn Phe Ser Thr Leu Trp			
350	355	360	
gtt cga aga gtt ttt agc ctt ata ggg atg att gga cct gcg ata ttc			1217
Val Arg Arg Val Phe Ser Leu Ile Gly Met Ile Gly Pro Ala Ile Phe			
365	370	375	
ctg gtt gcc gca gga ttt ata ggc tgt gat tat tcc ttg gct gtt gca			1265
Leu Val Ala Ala Gly Phe Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala			
380	385	390	
ttc cta acc ata tca aca acc ctg gga ggc ttt tgc tct tct gga ttt			1313
Phe Leu Thr Ile Ser Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe			
395	400	405	410
agc atc aac cat ctg gac att gct cct tcg tat gct ggt att ctc ctg			1361
Ser Ile Asn His Leu Asp Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu			
415	420	425	
ggc atc aca aat acc ttt gcc act att cct gga atg att ggg ccc atc			1409
Gly Ile Thr Asn Thr Phe Ala Thr Ile Pro Gly Met Ile Gly Pro Ile			
430	435	440	
att gcc aga agt ctt acc cct gag aac act att gga gaa tgg caa act			1457
Ile Ala Arg Ser Leu Thr Pro Glu Asn Thr Ile Gly Glu Trp Gln Thr			
445	450	455	
gtt ttc tgc atc gct gct atc aat gta ttt ggt gcc att ttc ttc			1505
Val Phe Cys Ile Ala Ala Ile Asn Val Phe Gly Ala Ile Phe Phe			
460	465	470	
aca cta ttc gcc aaa ggt gaa gtg caa aac tgg gcc atc agt gat cac			1553
Thr Leu Phe Ala Lys Gly Glu Val Gln Asn Trp Ala Ile Ser Asp His			
475	480	485	490
caa gga cac aga aac tgaaggaacc aataaataat cctgtctcta ttaatgtatc			1608
Gln Gly His Arg Asn			
495			

tttgttatac atgtaaccta aaagtgcctt tgatattta atgtgtaagc aatctatata 1668
caagataaaa ttgtactaga aaaattgtgt tagatttgcg aggcttgcg tcatgaaatg 1728
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gcttaattaa ggtggataat aattctcagg tcttgtaaa catctgttt tgcacacctt 1968
cctcaaaaaaa ttatttgcg tcaatcc ctgacatgta ggtctcaaac tttagcctct 2028
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<212> PRT
<213> Ovis sp.

<400> 4

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Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Phe Leu Ser Phe Phe
35 40 45

Gly Phe Phe Val Leu Tyr Ser Leu Arg Val Asn Leu Ser Val Ala Leu
50 55 60

Val Asp Met Val Asp Ser Asn Thr Thr Ala Lys Asp Asn Arg Thr Ser
65 70 75 80

Tyr Glu Cys Ala Glu His Ser Ala Pro Ile Lys Val Leu His Asn Gln
85 90 95

Thr Gly Lys Lys Tyr Arg Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu
100 105 110

Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr
115 120 125

Val Ala Ser Arg Ser Gly Gly Lys Leu Leu Leu Gly Phe Gly Ile Phe
130 135 140

Ala Thr Ala Ile Phe Thr Leu Phe Thr Pro Leu Ala Ala Asp Phe Gly
145 150 155 160

Val Gly Ala Leu Val Ala Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly
165 170 175

Val Thr Tyr Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro
180 185 190

Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu
195 200 205

Gly Thr Val Val Ser Leu Pro Leu Ser Gly Val Ile Cys Tyr Tyr Met
210 215 220

Asn Trp Thr Tyr Val Phe Tyr Phe Phe Gly Ile Val Gly Ile Ile Trp
225 230 235 240

Phe Ile Leu Trp Ile Cys Leu Val Ser Asp Thr Pro Glu Thr His Lys
245 250 255

Thr Ile Thr Pro Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Lys Asn
260 265 270

Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Ile Pro Met Leu Lys Ser
275 280 285

Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr
290 295 300

Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Val Leu
305 310 315 320

Arg Phe Asn Ile Gln Glu Asn Gly Phe Leu Ser Ala Val Pro Tyr Leu
325 330 335

Gly Cys Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn, Leu
340 345 350

Arg Ala Arg Trp Asn Phe Ser Thr Leu Trp Val Arg Arg Val Phe Ser
355 360 365

Leu Ile Gly Met Ile Gly Pro Ala Ile Phe Leu Val Ala Ala Gly Phe
370 375 380

Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr
385 390 395 400

Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp
405 410 415

Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe
420 425 430

Ala Thr Ile Pro Gly Met Ile Gly Pro Ile Ile Ala Arg Ser Leu Thr
435 440 445

Pro Glu Asn Thr Ile Gly Glu Trp Gln Thr Val Phe Cys Ile Ala Ala
450 455 460

Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly
465 470 475 480

Glu Val Gln Asn Trp Ala Ile Ser Asp His Gln Gly His Arg Asn
485 490 495

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR primer

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<212> DNA
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<223> Description of Artificial Sequence: PCR primer

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29

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<213> Homo sapiens

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gcgggagacg gtcgtccgaa caccggctcc ccggcatgcg tagaccggcg ggccggagcgg 180
gctcaactttg cgccaaatcct acgagaactc ccagaactcc gcttccctag tccaacccaa 240
gccagagttg cccacaccta ag atg gcg gcg ggg gcg atg aca ccg ccc cgc 292
Met Ala Ala Gly Ala Met Thr Pro Pro Arg
1 5 10

ccg gtc cag cca gct cgg ccc ggg ggc ttc ggg ctg tcg ggc cgg cgc 340
Pro Val Gln Pro Ala Arg Pro Gly Gly Phe Gly Leu Ser Gly Arg Arg
15 20 25

tcc ctt ctc tgc cag gtg gcg agt aca cct gct cac gta ggc gtc atg	388		
Ser Leu Leu Cys Gln Val Ala Ser Thr Pro Ala His Val Gly Val Met			
30	35	40	
agg tct ccg gtt cga gac ctg gcc cg aac gat ggc gag gag agc acg	436		
Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser Thr			
45	50	55	
gac cgc acg cct ctt cta ccg ggc gcc cca cg gaa gcc gct cca	484		
Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala Pro			
60	65	70	
gtg tgc tgc tct gct cgt tac aac tta gca att ttg gcc ttt ttt ggt	532		
Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe Gly			
75	80	85	90
tcc ttc att gtg tat gca tta cgt gtg aat ctg agt gtt gcg tta gtg	580		
Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu Val			
95	100	105	
gat atg gta gat tca aat aca act tta gaa gat aat aga act tcc aag	628		
Asp Met Val Asp Ser Asn Thr Thr Leu Glu Asp Asn Arg Thr Ser Lys			
110	115	120	
gcg tgt cca gag cat tct gct ccc ata aaa gtt cat cat aat caa acg	676		
Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln Thr			
125	130	135	
ggt aag aag tac caa tgg gat gca gaa act caa gga tgg att ctc ggt	724		
Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu Gly			
140	145	150	
tcc ttt ttt tat ggc tac atc atc aca cag att cct gga gga tat gtt	772		
Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr Val			
155	160	165	170
gcc agc aaa ata ggg ggg aaa atg ctg cta gga ttt ggg atc ctt ggc	820		
Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu Gly			
175	180	185	
act gct gtc ctc acc ctg ttc act ccc att gct gca gat tta gga gtt	868		
Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly Val			
190	195	200	
gga cca ctc att gta ctc aga gca cta gaa gga cta gga gag ggt gtt	916		
Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly Val			
205	210	215	

aca ttt cca gcc atg cat gcc atg tgg tct tct tgg gct ccc cct ctt			964
Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro Leu			
220	225	230	
gaa aga agc aaa ctt ctt agc att tcg tat gca gga gca cag ctt ggg			1012
Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu Gly			
235	240	245	250
aca gta att tct ctt cct ctt tct gga ata att tgc tac tat atg aat			1060
Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met Asn			
255	260	265	
tgg act tat gtc ttc tac ttt ttt ggt act att gga ata ttt tgg ttt			1108
Trp Thr Tyr Val Phe Tyr Phe Gly Thr Ile Gly Ile Phe Trp Phe			
270	275	280	
ctt ttg tgg atc tgg tta gtt agt gac aca cca caa aaa cac aag aga			1156
Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys Arg			
285	290	295	
att tcc cat tat gaa aag gaa tac att ctt tca tca tta aga aat cag			1204
Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn Gln			
300	305	310	
ctt tct tca cag aag tca gtg ccg tgg gta ccc att tta aaa tcc ctg			1252
Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser Leu			
315	320	325	330
cca ctt tgg gct atc gta gtt gca cac ttt tct tac aac tgg act ttt			1300
Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr Phe			
335	340	345	
tat act tta ttg aca tta ttg cct act tat atg aag gag atc cta agg			1348
Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu Arg			
350	355	360	
ttc aat gtt caa gag aat ggg ttt tta tct tca ttg cct tat tta ggc			1396
Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu Gly			
365	370	375	
tct tgg tta tgt atg atc ctg tct ggt caa gct gct gac aat tta agg			1444
Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu Arg			
380	385	390	
gca aaa tgg aat ttt tca act tta tgt gtt cgc aga att ttt agc ctt			1492
Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser Leu			
395	400	405	410

ata gga atg att gga cct gca gta ttc ctg gta gct gct ggc ttc att			1540
Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe Ile			
415	420	425	
ggc tgt gat tat tct ttg gcc gtt gct ttc cta act ata tca aca aca			1588
Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr Thr			
430	435	440	
ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat att			1636
Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp Ile			
445	450	455	
gct cct tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt gcc			1684
Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala			
460	465	470	
act att cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc cct			1732
Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro			
475	480	485	490
gat aac act gtt gga gaa tgg caa acc gtg ttc tat att gct gct gct			1780
Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala			
495	500	505	
att aat gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt gaa			1828
Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu			
510	515	520	
gta caa aac tgg gct ctc aat gat cac cat gga cac aga cac			1870
Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His			
525	530	535	
tgaaggaacc aataaataat cctgcctcta ttaatgtatt tttatttatac atgtAACCTC 1930			
aaagtgcctt ctgtattgtg taagcattct atgtttttt ttaattgtac ttgtattaga 1990			
ttttaaggc ctataatcat gaaatatcac tagtgccag aataataaaa tgaactgtgt 2050			
ttaattatga ataatatgtt agctaggact tctacttttag gttcacatac ctgcctgcta 2110			
gtcgggcaac atgaagttagg acagttctgt tgattttta gggccatact aaaggaaatg 2170			
agctgaaaca gacccctga taccttgct taattaaact agatgataat tctcaggtac 2230			
tgataaacac ctgttgggt tcactttcct cataaaaatt gtcagctctc tctgacactt 2290			
agacctcaaa cttagcatc tctgtggagc tgccatccac tgtataattt cgccctggcaa 2350			

ctggactgag gggagtgtgc ccaggcagct gccaagcact ccctccctgg cttcagggtc 2410
agagtgccca gcgttatca gaggcagcat ccaagcccag agccagtgtc gactttcg 2470
ctgggcctt tcctctgagg ggctatcaat gtgttagataa agccctgagt aggcaagagc 2530
agtgagatcc actgctatgg tcttgataca tcctcaaact ttcccttccc agcacagagg 2590
aatattggct ggcattgcaac ctgaaaaga aaaatgcgaa gcggccgggc acggggctc 2650
atgcctgtaa tcccagcact ttggggggct gaggtggcg aatcatgaga tcaggagttc 2710
gagaccagcc tggccagcat ggtgaaaccc catctctact aaaaatacaa aaaaattagct 2770
gggcgtggtg acgggcgcct gtaatcccag atactcagga ggctgaggta ggagaatcac 2830
ttgaacctgg gaggtggaag ttgcagtgaa ccaagatcac gccactgcac tccagcctgg 2890
gcgatggagc gagactccaa ctcaaaaaaa aaaaaaaaaa 2930

<210> 8
<211> 536
<212> PRT
<213> Homo sapiens

<400> 8
Met Ala Ala Gly Ala Met Thr Pro Pro Arg Pro Val Gln Pro Ala Arg
1 5 10 15

Pro Gly Gly Phe Gly Leu Ser Gly Arg Arg Ser Leu Leu Cys Gln Val
20 25 30

Ala Ser Thr Pro Ala His Val Gly Val Met Arg Ser Pro Val Arg Asp
35 40 45

Leu Ala Arg Asn Asp Gly Glu Glu Ser Thr Asp Arg Thr Pro Leu Leu
50 55 60

Pro Gly Ala Pro Arg Ala Glu Ala Ala Pro Val Cys Cys Ser Ala Arg
65 70 75 80

Tyr Asn Leu Ala Ile Leu Ala Phe Phe Gly Phe Phe Ile Val Tyr Ala
85 90 95

Leu Arg Val Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn
100 105 110

Thr Thr Leu Glu Asp Asn Arg Thr Ser Lys Ala Cys Pro Glu His Ser
115 120 125

Ala Pro Ile Lys Val His His Asn Gln Thr Gly Lys Lys Tyr Gln Trp
130 135 140

Asp Ala Glu Thr Gln Gly Trp Ile Leu Gly Ser Phe Phe Tyr Gly Tyr
145 150 155 160

Ile Ile Thr Gln Ile Pro Gly Gly Tyr Val Ala Ser Lys Ile Gly Gly
165 170 175

Lys Met Leu Leu Gly Phe Gly Ile Leu Gly Thr Ala Val Leu Thr Leu
180 185 190

Phe Thr Pro Ile Ala Ala Asp Leu Gly Val Gly Pro Leu Ile Val Leu
195 200 205

Arg Ala Leu Glu Gly Leu Gly Glu Gly Val Thr Phe Pro Ala Met His
210 215 220

Ala Met Trp Ser Ser Trp Ala Pro Pro Leu Glu Arg Ser Lys Leu Leu
225 230 235 240

Ser Ile Ser Tyr Ala Gly Ala Gln Leu Gly Thr Val Ile Ser Leu Pro
245 250 255

Leu Ser Gly Ile Ile Cys Tyr Tyr Met Asn Trp Thr Tyr Val Phe Tyr
260 265 270

Phe Phe Gly Thr Ile Gly Ile Phe Trp Phe Leu Leu Trp Ile Trp Leu
275 280 285

Val Ser Asp Thr Pro Gln Lys His Lys Arg Ile Ser His Tyr Glu Lys
290 295 300

Glu Tyr Ile Leu Ser Ser Leu Arg Asn Gln Leu Ser Ser Gln Lys Ser
305 310 315 320

Val Pro Trp Val Pro Ile Leu Lys Ser Leu Pro Leu Trp Ala Ile Val
325 330 335

Val Ala His Phe Ser Tyr Asn Trp Thr Phe Tyr Thr Leu Leu Thr Leu
340 345 350

Leu Pro Thr Tyr Met Lys Glu Ile Leu Arg Phe Asn Val Gln Glu Asn
355 360 365

Gly Phe Leu Ser Ser Leu Pro Tyr Leu Gly Ser Trp Leu Cys Met Ile
370 375 380

Leu Ser Gly Gln Ala Ala Asp Asn Leu Arg Ala Lys Trp Asn Phe Ser
385 390 395 400

Thr Leu Cys Val Arg Arg Ile Phe Ser Leu Ile Gly Met Ile Gly Pro
405 410 415

Ala Val Phe Leu Val Ala Ala Gly Phe Ile Gly Cys Asp Tyr Ser Leu
420 425 430

Ala Val Ala Phe Leu Thr Ile Ser Thr Thr Leu Gly Gly Phe Cys Ser
435 440 445

Ser Gly Phe Ser Ile Asn His Leu Asp Ile Ala Pro Ser Tyr Ala Gly
450 455 460

Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile Pro Gly Met Val
465 470 475 480

Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn Thr Val Gly Glu
485 490 495

Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn Val Phe Gly Ala
500 505 510

Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln Asn Trp Ala Leu
515 520 525

Asn Asp His His Gly His Arg His
530 535

<210> 9

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human/sheep
consensus sequence

<220>

<221> CDS

<222> (1)...(1485)

<400> 9

atg arg tcy ccg gtt ysr gac ytr gcc csg arc gay ggc gag gag rgc 48
 Met Xaa Xaa Pro Val Xaa Asp Xaa Ala Xaa Xaa Gly Glu Glu Xaa
 1 5 10 15

wcg gac cgc acr cck cty ctr cmg sgc gcc ccr cgg gcs gaa scc gct 96
 Xaa Asp Arg Xaa Xaa Xaa Xaa Xaa Ala Xaa Arg Xaa Glu Xaa Ala
 20 25 30

cca gtr tgc tgc tct gct cgt tac aac yta gca wtt ttg kcc ttt ttt 144
 Pro Xaa Cys Cys Ser Ala Arg Tyr Asn Xaa Ala Xaa Leu Xaa Phe Phe
 35 40 45

ggt ttc ttc rtt sts tat kca tta cgk gtg aat ctg agy gtt gcr yta 192
 Gly Phe Phe Xaa Xaa Tyr Xaa Leu Xaa Val Asn Leu Xaa Val Xaa Xaa
 50 55 60

gtg gay atg gtr gat tca aay aca act kym raa gat aat aga ack tcc 240
 Val Xaa Met Xaa Asp Ser Xaa Thr Thr Xaa Xaa Asp Asn Arg Xaa Ser
 65 70 75 80

was gmg tgt sca gag cat tct gct ccc ata aaa gtt cwt cay aay caa 288
 Xaa Xaa Cys Xaa Glu His Ser Ala Pro Ile Lys Val Xaa Xaa Xaa Gln
 85 90 95

acg ggt aar aag tac crr tgg gat gca gaa act caa gga tgg att ctc 336
 Thr Gly Xaa Lys Tyr Xaa Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu
 100 105 110

ggw tcy ttt tty tat ggc tac atc atc aca car att cct gga gga tat 384
 Xaa Xaa Phe Xaa Tyr Gly Tyr Ile Ile Thr Xaa Ile Pro Gly Gly Tyr
 115 120 125

gtt gcc agc ara akw ggg ggg aar mtg ytg cta gga tty ggg atc ytt 432
 Val Ala Ser Xaa Xaa Gly Gly Xaa Xaa Xaa Leu Gly Xaa Gly Ile Xaa
 130 135 140

gsy acw gct rtc ytc acc ctg ttc act ccc mty gct gca gat ttm gga 480
 Xaa Xaa Ala Xaa Xaa Thr Leu Phe Thr Pro Xaa Ala Ala Asp Xaa Gly
 145 150 155 160

gty gga scm cty rtt gya ctc agr gca cta gaa ggr cta gga gag ggt 528
 Xaa Gly Xaa Xaa Xaa Leu Xaa Ala Leu Glu Xaa Leu Gly Glu Gly
 165 170 175

gty aca twt cca gcc atg cat gcc atg tgg tct tcw tgg gct ccc cct 576
 Xaa Thr Xaa Pro Ala Met His Ala Met Trp Ser Xaa Trp Ala Pro Pro
 180 185 190

ctt gaa aga agc aar ctt ctk agy att tcr tat gca gga gca car ctt	624		
Leu Glu Arg Ser Xaa Leu Xaa Xaa Ile Xaa Tyr Ala Gly Ala Xaa Leu			
195	200	205	
ggg aca gta rtt tct ctt cct tct gga rta att tgc tac tat atg	672		
Gly Thr Val Xaa Ser Leu Pro Leu Ser Gly Xaa Ile Cys Tyr Tyr Met			
210	215	220	
aat tgg act tat gtc ttc tay tty ttt ggy ayt rtt gga atm wty tgg	720		
Asn Trp Thr Tyr Val Phe Xaa Xaa Phe Xaa Xaa Xaa Gly Xaa Xaa Trp			
225	230	235	240
ttt mtt ttr tgg atc tgs tta gtt agt gay aca cca saa amw cac aag	768		
Phe Xaa Xaa Trp Ile Xaa Leu Val Ser Xaa Thr Pro Xaa Xaa His Lys			
245	250	255	
asa aty wcy cmy tat gaa aag gar tay att ctt tca tca tta ara aat	816		
Xaa Xaa Xaa Xaa Tyr Glu Lys Xaa Xaa Ile Leu Ser Ser Leu Xaa Asn			
260	265	270	
cag cty tct tca cag aag tca gtg ccg tgg rta ccy atk ytr aaa tcm	864		
Gln Xaa Ser Ser Gln Lys Ser Val Pro Trp Xaa Xaa Xaa Lys Xaa			
275	280	285	
ctg cca ctt tgg gct aty gtm gtt gca cay ttt tct tac aac tgg act	912		
Leu Pro Leu Trp Ala Xaa Xaa Val Ala Xaa Phe Ser Tyr Asn Trp Thr			
290	295	300	
ttt tat act ttr ttg acm tta ttg cct act tay atg aag gar rtc cta	960		
Phe Tyr Thr Xaa Leu Xaa Leu Leu Pro Thr Xaa Met Lys Xaa Xaa Leu			
305	310	315	320
agg ttc aat rtt caa gag aat ggg ttt tta tct kca kts cct tat tta	1008		
Arg Phe Asn Xaa Gln Glu Asn Gly Phe Leu Ser Xaa Xaa Pro Tyr Leu			
325	330	335	
ggy tst tgg tta tgt atg atc ctg tck ggt caa gct gct gac aat tta	1056		
Xaa Xaa Trp Leu Cys Met Ile Leu Xaa Gly Gln Ala Ala Asp Asn Leu			
340	345	350	
agg gca ara tgg aat ttt tca act ytr tgk gtt cgm aga rtt ttt agc	1104		
Arg Ala Xaa Trp Asn Phe Ser Thr Xaa Xaa Val Xaa Arg Xaa Phe Ser			
355	360	365	
ctt ata ggr atg att gga cct gcr rta ttc ctg gtw gcy gcw ggm tty	1152		
Leu Ile Xaa Met Ile Gly Pro Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa Xaa			
370	375	380	

atw ggc tgt gat tat tcy ttg gcy gtt gcw ttc cta acy ata tca aca 1200
Xaa Gly Cys Asp Tyr Xaa Leu Xaa Val Xaa Phe Leu Xaa Ile Ser Thr
385 390 395 400

acm ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gay 1248
Xaa Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Xaa
405 410 415

att gct cct tcg tat gct ggt aty ctc ctg ggc atc aca aat acm ttt 1296
Ile Ala Pro Ser Tyr Ala Gly Xaa Leu Leu Gly Ile Thr Asn Xaa Phe
420 425 430

gcc act att ccw gga atg rtt ggg ccc rtc att gcy ara agt ctk acc 1344
Ala Thr Ile Xaa Gly Met Xaa Gly Pro Xaa Ile Xaa Xaa Ser Xaa Thr
435 440 445

cct gak aac act rtt gga gaa tgg caa acy gtk ttc try aty gct gct 1392
Pro Xaa Asn Thr Xaa Gly Glu Trp Gln Xaa Xaa Phe Xaa Xaa Ala Ala
450 455 460

gct aty aat gtw ttt ggt gcc att ttc tty aca cta ttc gcc aaa ggt 1440
Ala Xaa Asn Xaa Phe Gly Ala Ile Phe Xaa Thr Leu Phe Ala Lys Gly
465 470 475 480

gaa gtr caa aac tgg gcy mtc art gat cac caw gga cac aga mac 1485
Glu Xaa Gln Asn Trp Xaa Xaa Asp His Xaa Gly His Arg Xaa
485 490 495

<210> 10

<211> 495

<212> PRT

<213> Artificial Sequence

<400> 10

Met Xaa Xaa Pro Val Xaa Asp Xaa Ala Xaa Xaa Xaa Gly Glu Xaa
1 5 10 15

Xaa Asp Arg Xaa Xaa Xaa Xaa Xaa Ala Xaa Arg Xaa Glu Xaa Ala
20 25 30

Pro Xaa Cys Cys Ser Ala Arg Tyr Asn Xaa Ala Xaa Leu Xaa Phe Phe
35 40 45

Gly Phe Phe Xaa Xaa Tyr Xaa Leu Xaa Val Asn Leu Xaa Val Xaa Xaa
50 55 60

Val	Xaa	Met	Xaa	Asp	Ser	Xaa	Thr	Thr	Xaa	Xaa	Asp	Asn	Arg	Xaa	Ser
65				70					75					80	
Xaa Xaa Cys Xaa Glu His Ser Ala Pro Ile Lys Val Xaa Xaa Xaa Gln															
	85				90					95					
Thr Gly Xaa Lys Tyr Xaa Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu															
	100			105					110						
Xaa Xaa Phe Xaa Tyr Gly Tyr Ile Ile Thr Xaa Ile Pro Gly Gly Tyr															
	115			120					125						
Val Ala Ser Xaa Xaa Gly Gly Xaa Xaa Xaa Leu Gly Xaa Gly Ile Xaa															
	130			135					140						
Xaa Xaa Ala Xaa Xaa Thr Leu Phe Thr Pro Xaa Ala Ala Asp Xaa Gly															
	145			150					155				160		
Xaa Gly Xaa Xaa Xaa Xaa Leu Xaa Ala Leu Glu Xaa Leu Gly Glu Gly															
	165			170					175						
Xaa Thr Xaa Pro Ala Met His Ala Met Trp Ser Xaa Trp Ala Pro Pro															
	180			185					190						
Leu Glu Arg Ser Xaa Leu Xaa Xaa Ile Xaa Tyr Ala Gly Ala Xaa Leu															
	195			200					205						
Gly Thr Val Xaa Ser Leu Pro Leu Ser Gly Xaa Ile Cys Tyr Tyr Met															
	210			215					220						
Asn Trp Thr Tyr Val Phe Xaa Xaa Phe Xaa Xaa Xaa Gly Xaa Xaa Trp															
	225			230					235				240		
Phe Xaa Xaa Trp Ile Xaa Leu Val Ser Xaa Thr Pro Xaa Xaa His Lys															
	245			250					255						
Xaa Xaa Xaa Xaa Tyr Glu Lys Xaa Xaa Ile Leu Ser Ser Leu Xaa Asn															
	260			265					270						
Gln Xaa Ser Ser Gln Lys Ser Val Pro Trp Xaa Xaa Xaa Xaa Lys Xaa															
	275			280					285						
Leu Pro Leu Trp Ala Xaa Xaa Val Ala Xaa Phe Ser Tyr Asn Trp Thr															
	290			295					300						
Phe Tyr Thr Xaa Leu Xaa Leu Leu Pro Thr Xaa Met Lys Xaa Xaa Leu															
	305			310					315				320		

Arg Phe Asn Xaa Gln Glu Asn Gly Phe Leu Ser Xaa Xaa Pro Tyr Leu
325 330 335

Xaa Xaa Trp Leu Cys Met Ile Leu Xaa Gly Gln Ala Ala Asp Asn Leu
340 345 350

Arg Ala Xaa Trp Asn Phe Ser Thr Xaa Xaa Val Xaa Arg Xaa Phe Ser
355 360 365

Leu Ile Xaa Met Ile Gly Pro Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa
370 375 380

Xaa Gly Cys Asp Tyr Xaa Leu Xaa Val Xaa Phe Leu Xaa Ile Ser Thr
385 390 395 400

Xaa Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Xaa
405 410 415

Ile Ala Pro Ser Tyr Ala Gly Xaa Leu Leu Gly Ile Thr Asn Xaa Phe
420 425 430

Ala Thr Ile Xaa Gly Met Xaa Gly Pro Xaa Ile Xaa Xaa Ser Xaa Thr
435 440 445

Pro Xaa Asn Thr Xaa Gly Glu Trp Gln Xaa Xaa Phe Xaa Xaa Ala Ala
450 455 460

Ala Xaa Asn Xaa Phe Gly Ala Ile Phe Xaa Thr Leu Phe Ala Lys Gly
465 470 475 480

Glu Xaa Gln Asn Trp Xaa Xaa Asp His Xaa Gly His Arg Xaa
485 490 495

<210> 11
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human/sheep
consensus sequence

<220>
<221> CDS
<222> (1)..(1485)

<400> 11

atg ang tcn ccg gtt nnn gac ntn gcc cng anc gan ggc gag gag ngc Met Xaa Xaa Pro Val Xaa Asp Xaa Ala Xaa Xaa Xaa Gly Glu Glu Xaa	1	5	10	15	48
ncg gac cgc acn ccn ctn ctn cng nge gcc ccn cgg gcn gaa ncc gct Xaa Asp Arg Xaa Xaa Xaa Xaa Xaa Ala Xaa Arg Xaa Glu Xaa Ala	20	25		30	96
cca gtn tgc tgc tct gct cgt tac aac nta gca ntt ttg ncc ttt ttt Pro Xaa Cys Cys Ser Ala Arg Tyr Asn Xaa Ala Xaa Leu Xaa Phe Phe	35	40	45		144
ggt ttc ttc ntt ntn tat nca tta cgn gtg aat ctg agn gtt gcn nta Gly Phe Phe Xaa Xaa Tyr Xaa Leu Xaa Val Asn Leu Xaa Val Xaa Xaa	50	55	60		192
gtg gan atg gtn gat tca aan aca act nnn naa gat aat aga acn tcc Val Xaa Met Xaa Asp Ser Xaa Thr Thr Xaa Xaa Asp Asn Arg Xaa Ser	65	70	75	80	240
nan gng tgt nca gag cat tct gct ccc ata aaa gtt cnt can aan caa Xaa Xaa Cys Xaa Glu His Ser Ala Pro Ile Lys Val Xaa Xaa Xaa Gln	85	90		95	288
acg ggt aan aag tac cnc tgg gat gca gaa act caa gga tgg att ctc Thr Gly Xaa Lys Tyr Xaa Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu	100	105		110	336
ggn tcn ttt ttn tat ggc tac atc atc aca can att cct gga gga tat Xaa Xaa Phe Xaa Tyr Gly Tyr Ile Ile Thr Xaa Ile Pro Gly Gly Tyr	115	120	125		384
gtt gcc agc ana ann ggg ggg aan ntg ntg cta gga ttn ggg atc ntt Val Ala Ser Xaa Xaa Gly Gly Xaa Xaa Xaa Leu Gly Xaa Gly Ile Xaa	130	135	140		432
gnn acn gct ntc ntc acc ctg ttc act ccc ntn gct gca gat ttn gga Xaa Xaa Ala Xaa Xaa Thr Leu Phe Thr Pro Xaa Ala Ala Asp Xaa Gly	145	150	155	160	480
gtn gga ncn ctn ntt gna ctc agn gca cta gaa ggn cta gga gag ggt Xaa Gly Xaa Xaa Xaa Leu Xaa Ala Leu Glu Xaa Leu Gly Glu Gly	165	170	175		528
gtn aca tnt cca gcc atg cat gcc atg tgg tct tcn tgg gct ccc cct Xaa Thr Xaa Pro Ala Met His Ala Met Trp Ser Xaa Trp Ala Pro Pro	180	185	190		576

ctt gaa aga agc aan ctt ctn agn att tcn tat gca gga gca can ctt			624
Leu Glu Arg Ser Xaa Leu Xaa Xaa Ile Xaa Tyr Ala Gly Ala Xaa Leu			
195	200	205	
ggg aca gta ntt tct ctt cct tct gga nta att tgc tac tat atg			672
Gly Thr Val Xaa Ser Leu Pro Leu Ser Gly Xaa Ile Cys Tyr Tyr Met			
210	215	220	
aat tgg act tat gtc ttc tan ttn ttt ggn ant ntt gga atn ntn tgg			720
Asn Trp Thr Tyr Val Phe Xaa Xaa Phe Xaa Xaa Xaa Gly Xaa Xaa Trp			
225	230	235	240
ttt ntt ttn tgg atc tgn tta gtt agt gan aca cca naa ann cac aag			768
Phe Xaa Xaa Trp Ile Xaa Leu Val Ser Xaa Thr Pro Xaa Xaa His Lys			
245	250	255	
ana atn ncn tat gaa aag gan tan att ctt tca tca tta ana aat			816
Xaa Xaa Xaa Xaa Tyr Glu Lys Xaa Xaa Ile Leu Ser Ser Leu Xaa Asn			
260	265	270	
cag ctn tct tca cag aag tca gtg ccg tgg nta ccn atn ntn aaa tcn			864
Gln Xaa Ser Ser Gln Lys Ser Val Pro Trp Xaa Xaa Xaa Xaa Lys Xaa			
275	280	285	
ctg cca ctt tgg gct atn gtn gtt gca can ttt tct tac aac tgg act			912
Leu Pro Leu Trp Ala Xaa Xaa Val Ala Xaa Phe Ser Tyr Asn Trp Thr			
290	295	300	
ttt tat act ttn ttg acn tta ttg cct act tan atg aag gan ntc cta			960
Phe Tyr Thr Xaa Leu Xaa Leu Leu Pro Thr Xaa Met Lys Xaa Xaa Leu			
305	310	315	320
agg ttc aat ntt caa gag aat ggg ttt tta tct nca ntn cct tat tta			1008
Arg Phe Asn Xaa Gln Glu Asn Gly Phe Leu Ser Xaa Xaa Pro Tyr Leu			
325	330	335	
ggn tnt tgg tta tgt atg atc ctg tcn ggt caa gct gct gac aat tta			1056
Xaa Xaa Trp Leu Cys Met Ile Leu Xaa Gly Gln Ala Ala Asp Asn Leu			
340	345	350	
agg gca ana tgg aat ttt tca act ntn tgn gtt cgn aga ntt ttt agc			1104
Arg Ala Xaa Trp Asn Phe Ser Thr Xaa Xaa Val Xaa Arg Xaa Phe Ser			
355	360	365	
ctt ata ggn atg att gga cct gcn nta ttc ctg gtn gcn gcn ggn ttn			1152
Leu Ile Xaa Met Ile Gly Pro Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa			
370	375	380	

atn ggc tgt gat tat tcn ttg gcn gtt gcn ttc cta acn ata tca aca Xaa Gly Cys Asp Tyr Xaa Leu Xaa Val Xaa Phe Leu Xaa Ile Ser Thr 385	390	395	400	1200
acn ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gan Xaa Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Xaa 405	410	415		1248
att gct cct tcg tat gct ggt atn ctc ctg ggc atc aca aat acn ttt Ile Ala Pro Ser Tyr Ala Gly Xaa Leu Leu Gly Ile Thr Asn Xaa Phe 420	425	430		1296
gcc act att ccn gga atg ntt ggg ccc ntc att gcn ana agt ctn acc Ala Thr Ile Xaa Gly Met Xaa Gly Pro Xaa Ile Xaa Xaa Ser Xaa Thr 435	440	445		1344
cct gan aac act ntt gga gaa tgg caa acn gtn ttc tnn atn gct gct Pro Xaa Asn Thr Xaa Gly Glu Trp Gln Xaa Xaa Phe Xaa Xaa Ala Ala 450	455	460		1392
gct atn aat gtn ttt ggt gcc att ttc ttn aca cta ttc gcc aaa ggt Ala Xaa Asn Xaa Phe Gly Ala Ile Phe Xaa Thr Leu Phe Ala Lys Gly 465	470	475	480	1440
gaa gtn caa aac tgg gcn ntc ant gat cac can gga cac aga nac Glu Xaa Gln Asn Trp Xaa Xaa Xaa Asp His Xaa Gly His Arg Xaa 485	490	495		1485

<210> 12

<211> 495

<212> PRT

<213> Artificial Sequence

<400> 12

Met Xaa Xaa Pro Val Xaa Asp Xaa Ala Xaa Xaa Xaa Gly Glu Xaa 1	5	10	15
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Xaa Asp Arg Xaa Xaa Xaa Xaa Xaa Ala Xaa Arg Xaa Glu Xaa Ala 20	25	30
---	----	----

Pro Xaa Cys Cys Ser Ala Arg Tyr Asn Xaa Ala Xaa Leu Xaa Phe Phe 35	40	45
---	----	----

Gly Phe Phe Xaa Xaa Tyr Xaa Leu Xaa Val Asn Leu Xaa Val Xaa Xaa 50	55	60
---	----	----

Val Xaa Met Xaa Asp Ser Xaa Thr Thr Xaa Xaa Asp Asn Arg Xaa Ser

65

70

75

80

Xaa Xaa Cys Xaa Glu His Ser Ala Pro Ile Lys Val Xaa Xaa Xaa Gln
 85 90 95

Thr Gly Xaa Lys Tyr Xaa Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu
 100 105 110

Xaa Xaa Phe Xaa Tyr Gly Tyr Ile Ile Thr Xaa Ile Pro Gly Gly Tyr
 115 120 125

Val Ala Ser Xaa Xaa Gly Gly Xaa Xaa Xaa Leu Gly Xaa Gly Ile Xaa
 130 135 140

Xaa Xaa Ala Xaa Xaa Thr Leu Phe Thr Pro Xaa Ala Ala Asp Xaa Gly
 145 150 155 160

Xaa Gly Xaa Xaa Xaa Xaa Leu Xaa Ala Leu Glu Xaa Leu Gly Glu Gly
 165 170 175

Xaa Thr Xaa Pro Ala Met His Ala Met Trp Ser Xaa Trp Ala Pro Pro
 180 185 190

Leu Glu Arg Ser Xaa Leu Xaa Xaa Ile Xaa Tyr Ala Gly Ala Xaa Leu
 195 200 205

Gly Thr Val Xaa Ser Leu Pro Leu Ser Gly Xaa Ile Cys Tyr Tyr Met
 210 215 220

Asn Trp Thr Tyr Val Phe Xaa Xaa Phe Xaa Xaa Xaa Gly Xaa Xaa Trp
 225 230 235 240

Phe Xaa Xaa Trp Ile Xaa Leu Val Ser Xaa Thr Pro Xaa Xaa His Lys
 245 250 255

Xaa Xaa Xaa Xaa Tyr Glu Lys Xaa Xaa Ile Leu Ser Ser Leu Xaa Asn
 260 265 270

Gln Xaa Ser Ser Gln Lys Ser Val Pro Trp Xaa Xaa Xaa Xaa Lys Xaa
 275 280 285

Leu Pro Leu Trp Ala Xaa Xaa Val Ala Xaa Phe Ser Tyr Asn Trp Thr
 290 295 300

Phe Tyr Thr Xaa Leu Xaa Leu Leu Pro Thr Xaa Met Lys Xaa Xaa Leu
 305 310 315 320

Arg Phe Asn Xaa Gln Glu Asn Gly Phe Leu Ser Xaa Xaa Pro Tyr Leu

325

330

335

Xaa Xaa Trp Leu Cys Met Ile Leu Xaa Gly Gln Ala Ala Asp Asn Leu
340 345 350

Arg Ala Xaa Trp Asn Phe Ser Thr Xaa Xaa Val Xaa Arg Xaa Phe Ser
355 360 365

Leu Ile Xaa Met Ile Gly Pro Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa
370 375 380

Xaa Gly Cys Asp Tyr Xaa Leu Xaa Val Xaa Phe Leu Xaa Ile Ser Thr
385 390 395 400

Xaa Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Xaa
405 410 415

Ile Ala Pro Ser Tyr Ala Gly Xaa Leu Leu Gly Ile Thr Asn Xaa Phe
420 425 430

Ala Thr Ile Xaa Gly Met Xaa Gly Pro Xaa Ile Xaa Xaa Ser Xaa Thr
435 440 445

Pro Xaa Asn Thr Xaa Gly Glu Trp Gln Xaa Xaa Phe Xaa Xaa Ala Ala
450 455 460

Ala Xaa Asn Xaa Phe Gly Ala Ile Phe Xaa Thr Leu Phe Ala Lys Gly
465 470 475 480

Glu Xaa Gln Asn Trp Xaa Xaa Xaa Asp His Xaa Gly His Arg Xaa
485 490 495